

SEQUENCE LISTING

<110> Reinhard, Christoph
Jefferson, Anne B.
Chan, Vivien W.

<120> TTK in Diagnosis and as a Therapeutic
Target in Cancer

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aca cag caa tcc acg cag gct act caa agg ttt ttg att gag aag ttt 102
Thr Gln Gln Ser Thr Gln Ala Thr Gln Arg Phe Leu Ile Glu Lys Phe
10 15 20

tct caa gaa cag atc ggc gaa aac att gtg tgc agg gtc att tgt acc 150
Ser Gln Glu Gln Ile Gly Glu Asn Ile Val Cys Arg Val Ile Cys Thr
25 30 35

acg ggt caa att ccc atc cga gat ttg tca gct gat att tca caa gtg 198
Thr Gly Gln Ile Pro Ile Arg Asp Leu Ser Ala Asp Ile Ser Gln Val
40 45 50 55

ctt aag gaa aaa cga tcc ata aag aaa gtt tgg aca ttt ggt aga aac 246
Leu Lys Glu Lys Arg Ser Ile Lys Lys Val Trp Thr Phe Gly Arg Asn
60 65 70

cca gcc tgt gac tat cat tta gga aac att tca aga ctg tca aat aag 294
Pro Ala Cys Asp Tyr His Leu Gly Asn Ile Ser Arg Leu Ser Asn Lys
75 80 85

cat ttc caa ata cta cta gga gaa gac ggt aac ctt tta ttg aat gac 342
His Phe Gln Ile Leu Leu Gly Glu Asp Gly Asn Leu Leu Leu Asn Asp
90 95 100

att tcc act aat ggg acc tgg tta aat ggg caa aaa gtc gag aag aac 390
Ile Ser Thr Asn Gly Thr Trp Leu Asn Gly Gln Lys Val Glu Lys Asn
105 110 115

agc aat cag tta ctg tct caa ggt gat gaa ata acc gtt ggt gta ggc 438
Ser Asn Gln Leu Leu Ser Gln Gly Asp Glu Ile Thr Val Gly Val Gly
120 125 130 135

gtg gaa tca gat att tta tct ctg gtc att ttc ata aac gac aaa ttt 486
Val Glu Ser Asp Ile Leu Ser Leu Val Ile Phe Ile Asn Asp Lys Phe
140 145 150

aag cag tgc ctc gag cag aac aaa gtt gat cgc ata aga tct aac ctg 534
Lys Gln Cys Leu Glu Gln Asn Lys Val Asp Arg Ile Arg Ser Asn Leu
155 160 165

aaa Lys	aat Asn	acc Thr 170	tct Ser	aaa Lys	ata Ile	gct Ala	tct Ser 175	cct Pro	ggt Gly	ctt Leu	aca Thr 180	tca Ser	tct Ser	act Thr	gca Ala	582
tca Ser 185	tca Ser	atg Met	gtg Val	gcc Ala	aac Asn	aag Lys 190	act Thr	ggt Gly	att Ile	ttt Phe 195	aag Lys 195	gat Asp	ttt Phe	tcg Ser	att Ile	630
att Ile 200	gac Asp	gaa Glu	gtg Val	gtg Val	ggc Gly 205	cag Gln	ggt Gly	gca Ala	ttt Phe	gcc Ala 210	aca Thr	gta Val	aag Lys	aaa Lys	gcc Ala 215	678
att Ile	gaa Glu	aga Arg	act Thr	act Thr 220	ggg Gly	aaa Lys	aca Thr	ttc Phe 225	gcg Ala	gtg Val	aag Lys	att Ile	ata Ile	agt Ser 230	aaa Lys	726
cgc Arg	aaa Lys	gta Val	ata Ile 235	ggc Gly	aat Asn	atg Met	gat Asp	ggt Gly 240	gtg Val	aca Thr	aga Arg	gag Glu 245	tta Leu 245	gaa Glu	gta Val	774
ttg Leu	caa Gln 250	aag Lys	ctc Leu	aat Asn	cat His	cca Pro	agg Arg 255	ata Ile	gta Val	cga Arg	ttg Leu 260	aaa Lys 260	gga Gly	ttt Phe	tat Tyr	822
gaa Glu 265	gat Asp	act Thr	gag Glu	agt Ser	tat Tyr	tat Tyr 270	atg Met	gtg Val	atg Met	gag Glu	ttc Phe 275	gtt Val	tct Ser	ggt Gly	ggt Gly	870
gac Asp 280	tta Leu	atg Met	gat Asp	ttt Phe	gtt Val 285	gct Ala	gct Ala	cat His	ggt Gly	gcg Ala 290	gtt Val	gga Gly	gaa Glu	gat Asp	gct Ala 295	918
ggg Gly	agg Arg	gag Glu	ata Ile	tcc Ser 300	agg Arg	cag Gln	ata Ile	ctc Leu	aca Thr 305	gca Ala	ata Ile	aaa Lys	tac Tyr	att Ile 310	cac His	966
tct Ser	atg Met	ggc Gly 315	atc Ile	agc Ser	cat His	cgt Arg	gac Asp	cta Leu 320	aag Lys	ccc Pro	gat Asp	aat Asn	att Ile 325	ctt Leu	att Ile	1014
gaa Glu	caa Gln 330	gac Asp	gat Asp	cct Pro	gta Val	ttg Leu	gta Val 335	aag Lys	ata Ile	acc Thr	gac Asp	ttt Phe 340	ggt Gly	ctg Leu	gca Ala	1062
aaa Lys 345	gta Val	caa Gln	gga Gly	aat Asn	ggg Gly	tct Ser 350	ttt Phe	atg Met	aaa Lys	acc Thr	ttc Phe 355	tgt Cys	ggc Gly	act Thr	ttg Leu	1110
gca Ala 360	tat Tyr	gtg Val	gca Ala	cct Pro	gaa Glu 365	gtc Val	atc Ile	aga Arg	ggt Gly	aaa Lys 370	gat Asp	aca Thr	tcc Ser	gta Val	tct Ser 375	1158
cct Pro	gat Asp	gaa Glu	tac Tyr	gaa Glu 380	gaa Glu	agg Arg	aat Asn	gag Glu	tac Tyr 385	tct Ser	tcg Ser	tta Leu	gtg Val	gat Asp 390	atg Met	1206

tgg tca atg gga tgt ctt gtg tat gtt atc cta acg ggc cac tta cct	1254
Trp Ser Met Gly Cys Leu Val Tyr Val Ile Leu Thr Gly His Leu Pro	
395 400 405	
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Phe Ser Gly Ser Thr Gln Asp Gln Leu Tyr Lys Gln Ile Gly Arg Gly	
410 415 420	
tca tat cat gaa ggg ccc ctc aaa gat ttc cgg ata tct gaa gaa gca	1350
Ser Tyr His Glu Gly Pro Leu Lys Asp Phe Arg Ile Ser Glu Glu Ala	
425 430 435	
aga gat ttc ata gat tca ttg tta cag gtg gat cca aat aat agg tcg	1398
Arg Asp Phe Ile Asp Ser Leu Leu Gln Val Asp Pro Asn Asn Arg Ser	
440 445 450 455	
aca gct gca aaa gcc ttg aat cat ccc tgg atc aag atg agt cca ttg	1446
Thr Ala Ala Lys Ala Leu Asn His Pro Trp Ile Lys Met Ser Pro Leu	
460 465 470	
ggc tca caa tca tat ggt gat ttt tca caa ata tcc tta tca caa tcg	1494
Gly Ser Gln Ser Tyr Gly Asp Phe Ser Gln Ile Ser Leu Ser Gln Ser	
475 480 485	
ttg tcg cag cag aaa tta tta gaa aat atg gac gat gct caa tac gaa	1542
Leu Ser Gln Gln Lys Leu Leu Glu Asn Met Asp Asp Ala Gln Tyr Glu	
490 495 500	
ttt gtc aaa gcg caa agg aaa tta caa atg gag caa caa ctt caa gaa	1590
Phe Val Lys Ala Gln Arg Lys Leu Gln Met Glu Gln Gln Leu Gln Glu	
505 510 515	
cag gat cag gaa gac caa gat gga aaa att caa gga ttt aaa ata ccc	1638
Gln Asp Gln Glu Asp Gln Asp Gly Lys Ile Gln Gly Phe Lys Ile Pro	
520 525 530 535	
gca cac gcc cct att cga tat aca cag ccc aaa agc att gaa gca gaa	1686
Ala His Ala Pro Ile Arg Tyr Thr Gln Pro Lys Ser Ile Glu Ala Glu	
540 545 550	
act aga gaa caa aaa ctt tta cat tcc aat aat act gag aat gtc aag	1734
Thr Arg Glu Gln Lys Leu Leu His Ser Asn Asn Thr Glu Asn Val Lys	
555 560 565	
agc tca aag aaa aag ggt aat ggt agg ttt tta act tta aaa cca ttg	1782
Ser Ser Lys Lys Lys Gly Asn Gly Arg Phe Leu Thr Leu Lys Pro Leu	
570 575 580	
cct gac agc att att caa gaa agc ctg gag att cag caa ggt gtg aat	1830
Pro Asp Ser Ile Ile Gln Glu Ser Leu Glu Ile Gln Gln Gly Val Asn	
585 590 595	
cca ttt ttc att ggt aga tcc gag gat tgc aat tgt aaa att gaa gac	1878
Pro Phe Phe Ile Gly Arg Ser Glu Asp Cys Asn Cys Lys Ile Glu Asp	
600 605 610 615	
aat agg ttg tct cga gtt cat tgc ttc att ttc aaa aag agg cat gct	1926

Asn	Arg	Leu	Ser	Arg	Val	His	Cys	Phe	Ile	Phe	Lys	Lys	Arg	His	Ala	
				620					625					630		
gta	ggc	aaa	agc	atg	tat	gaa	tct	ccg	gca	caa	ggc	tta	gat	gat	att	1974
Val	Gly	Lys	Ser	Met	Tyr	Glu	Ser	Pro	Ala	Gln	Gly	Leu	Asp	Asp	Ile	
			635					640					645			
tgg	tat	tgc	cac	acc	gga	act	aac	gtg	agc	tat	tta	aat	aat	aac	cgc	2022
Trp	Tyr	Cys	His	Thr	Gly	Thr	Asn	Val	Ser	Tyr	Leu	Asn	Asn	Asn	Arg	
		650					655					660				
atg	ata	cag	ggc	acg	aaa	ttc	ctt	tta	caa	gac	gga	gat	gaa	atc	aag	2070
Met	Ile	Gln	Gly	Thr	Lys	Phe	Leu	Leu	Gln	Asp	Gly	Asp	Glu	Ile	Lys	
	665					670					675					
atc	att	tgg	gat	aaa	aac	aat	aaa	ttt	gtc	att	ggc	ttt	aaa	gtg	gaa	2118
Ile	Ile	Trp	Asp	Lys	Asn	Asn	Lys	Phe	Val	Ile	Gly	Phe	Lys	Val	Glu	
680					685				690					695		
att	aac	gat	act	aca	ggc	ctg	ttt	aac	gag	gga	tta	ggc	atg	tta	caa	2166
Ile	Asn	Asp	Thr	Thr	Gly	Leu	Phe	Asn	Glu	Gly	Leu	Gly	Met	Leu	Gln	
			700					705					710			
gaa	caa	aga	gta	gta	ctt	aag	caa	aca	gcc	gaa	gaa	aaa	gat	ttg	gtg	2214
Glu	Gln	Arg	Val	Val	Leu	Lys	Gln	Thr	Ala	Glu	Glu	Lys	Asp	Leu	Val	
			715					720					725			
aaa	aag	tta	acc	cag	atg	atg	gca	gct	caa	cgt	gca	aat	caa	ccc	tcg	2262
Lys	Lys	Leu	Thr	Gln	Met	Met	Ala	Ala	Gln	Arg	Ala	Asn	Gln	Pro	Ser	
		730					735					740				
gct	tct	tct	tca	tca	atg	tcg	gct	aag	aag	ccg	cca	gtt	agc	gat	aca	2310
Ala	Ser	Ser	Ser	Ser	Met	Ser	Ala	Lys	Lys	Pro	Pro	Val	Ser	Asp	Thr	
	745					750					755					
aat	aat	aac	ggc	aat	aat	tcg	gta	cta	aac	gac	ttg	gta	gag	tca	ccg	2358
Asn	Asn	Asn	Gly	Asn	Asn	Ser	Val	Leu	Asn	Asp	Leu	Val	Glu	Ser	Pro	
760					765					770				775		
att	aat	gcg	aat	acg	ggg	aac	att	ttg	aag	aga	ata	cat	tcg	gta	agt	2406
Ile	Asn	Ala	Asn	Thr	Gly	Asn	Ile	Leu	Lys	Arg	Ile	His	Ser	Val	Ser	
				780				785						790		
tta	tcg	caa	tca	caa	att	gat	cct	agt	aag	aag	gtt	aaa	agg	gca	aaa	2454
Leu	Ser	Gln	Ser	Gln	Ile	Asp	Pro	Ser	Lys	Lys	Val	Lys	Arg	Ala	Lys	
			795					800					805			
ttg	gac	caa	acc	tca	aaa	ggc	ccc	gag	aat	ttg	caa	ttt	tcg	taa		2499
Leu	Asp	Gln	Thr	Ser	Lys	Gly	Pro	Glu	Asn	Leu	Gln	Phe	Ser	*		
	810						815					820				
ccaaggacaa	atacccatag	aaaatgctgc	cccttttttaa	gagagaagat	ggtagatacc											2559
aatactcaga	attcccagta	caaagaacca	atatcggagt	caataaacag	tatgatgaac											2619
ttgcttttcgc	aaataaaaga	tatcactcag	aagcaccag	taataaagga	tcgagatagc											2679
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<210> 16

<211> 821
 <212> PRT
 <213> Saccharomyces cerevisiae

<400> 16

Met	Glu	Asn	Ile	Thr	Gln	Pro	Thr	Gln	Gln	Ser	Thr	Gln	Ala	Thr	Gln
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			20					25					30		
Val	Cys	Arg	Val	Ile	Cys	Thr	Thr	Gly	Gln	Ile	Pro	Ile	Arg	Asp	Leu
		35					40					45			
Ser	Ala	Asp	Ile	Ser	Gln	Val	Leu	Lys	Glu	Lys	Arg	Ser	Ile	Lys	Lys
	50					55					60				
Val	Trp	Thr	Phe	Gly	Arg	Asn	Pro	Ala	Cys	Asp	Tyr	His	Leu	Gly	Asn
65					70					75					80
Ile	Ser	Arg	Leu	Ser	Asn	Lys	His	Phe	Gln	Ile	Leu	Leu	Gly	Glu	Asp
				85					90					95	
Gly	Asn	Leu	Leu	Leu	Asn	Asp	Ile	Ser	Thr	Asn	Gly	Thr	Trp	Leu	Asn
			100					105					110		
Gly	Gln	Lys	Val	Glu	Lys	Asn	Ser	Asn	Gln	Leu	Leu	Ser	Gln	Gly	Asp
		115					120					125			
Glu	Ile	Thr	Val	Gly	Val	Gly	Val	Glu	Ser	Asp	Ile	Leu	Ser	Leu	Val
	130					135					140				
Ile	Phe	Ile	Asn	Asp	Lys	Phe	Lys	Gln	Cys	Leu	Glu	Gln	Asn	Lys	Val
145					150					155					160
Asp	Arg	Ile	Arg	Ser	Asn	Leu	Lys	Asn	Thr	Ser	Lys	Ile	Ala	Ser	Pro
				165					170					175	
Gly	Leu	Thr	Ser	Ser	Thr	Ala	Ser	Ser	Met	Val	Ala	Asn	Lys	Thr	Gly
			180				185						190		
Ile	Phe	Lys	Asp	Phe	Ser	Ile	Ile	Asp	Glu	Val	Val	Gly	Gln	Gly	Ala
	195						200					205			
Phe	Ala	Thr	Val	Lys	Lys	Ala	Ile	Glu	Arg	Thr	Thr	Gly	Lys	Thr	Phe
	210					215					220				
Ala	Val	Lys	Ile	Ile	Ser	Lys	Arg	Lys	Val	Ile	Gly	Asn	Met	Asp	Gly
225					230					235					240
Val	Thr	Arg	Glu	Leu	Glu	Val	Leu	Gln	Lys	Leu	Asn	His	Pro	Arg	Ile
				245					250					255	
Val	Arg	Leu	Lys	Gly	Phe	Tyr	Glu	Asp	Thr	Glu	Ser	Tyr	Tyr	Met	Val
			260				265						270		
Met	Glu	Phe	Val	Ser	Gly	Gly	Asp	Leu	Met	Asp	Phe	Val	Ala	Ala	His
		275					280					285			
Gly	Ala	Val	Gly	Glu	Asp	Ala	Gly	Arg	Glu	Ile	Ser	Arg	Gln	Ile	Leu
	290					295					300				
Thr	Ala	Ile	Lys	Tyr	Ile	His	Ser	Met	Gly	Ile	Ser	His	Arg	Asp	Leu
305					310					315					320
Lys	Pro	Asp	Asn	Ile	Leu	Ile	Glu	Gln	Asp	Asp	Pro	Val	Leu	Val	Lys
			325						330					335	
Ile	Thr	Asp	Phe	Gly	Leu	Ala	Lys	Val	Gln	Gly	Asn	Gly	Ser	Phe	Met
			340				345						350		
Lys	Thr	Phe	Cys	Gly	Thr	Leu	Ala	Tyr	Val	Ala	Pro	Glu	Val	Ile	Arg
		355					360					365			
Gly	Lys	Asp	Thr	Ser	Val	Ser	Pro	Asp	Glu	Tyr	Glu	Glu	Arg	Asn	Glu
	370					375					380				
Tyr	Ser	Ser	Leu	Val	Asp	Met	Trp	Ser	Met	Gly	Cys	Leu	Val	Tyr	Val
385					390					395					400
Ile	Leu	Thr	Gly	His	Leu	Pro	Phe	Ser	Gly	Ser	Thr	Gln	Asp	Gln	Leu
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<213> Homo sapiens

<220>

<221> CDS

<222> (289)...(1230)

<400> 17

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tccgactcgc cctcggcctt ccgcgccagc cgcagccaca gccgcaacgc caccgcagc 180
cacagccaca gccacagccc caggcatagc cttcggcaca gccccggctc cggctcctgc 240
ggcagctcct ctgggcaccg tccctgcgcc gacatcctgg aggttggg atg ctc ttg 297
                                     Met Leu Leu
                                     1
```

```
tcc aaa atc aac tcg ctt gcc cac ctg cgc gcc gcg ccc tgc aac gac 345
Ser Lys Ile Asn Ser Leu Ala His Leu Arg Ala Ala Pro Cys Asn Asp
      5                      10                      15
```

```
ctg cac gcc acc aag ctg gcg ccc ggc aag gag aag gag ccc ctg gag 393
Leu His Ala Thr Lys Leu Ala Pro Gly Lys Glu Lys Glu Pro Leu Glu
      20                      25                      30                      35
```

```
tcg cag tac cag gtg ggc ccg cta ctg ggc agc ggc ggc ttc ggc tcg 441
Ser Gln Tyr Gln Val Gly Pro Leu Leu Gly Ser Gly Gly Phe Gly Ser
                      40                      45                      50
```

```
gtc tac tca ggc atc cgc gtc tcc gac aac ttg ccg gtg gcc atc aaa 489
Val Tyr Ser Gly Ile Arg Val Ser Asp Asn Leu Pro Val Ala Ile Lys
                      55                      60                      65
```

```
cac gtg gag aag gac cgg att tcc gac tgg gga gag ctg cct aat ggc 537
His Val Glu Lys Asp Arg Ile Ser Asp Trp Gly Glu Leu Pro Asn Gly
                      70                      75                      80
```

```
act cga gtg ccc atg gaa gtg gtc ctg ctg aag aag gtg agc tcg ggt 585
Thr Arg Val Pro Met Glu Val Val Leu Leu Lys Lys Val Ser Ser Gly
      85                      90                      95
```

```
ttc tcc ggc gtc att agg ctc ctg gac tgg ttc gag agg ccc gac agt 633
Phe Ser Gly Val Ile Arg Leu Leu Asp Trp Phe Glu Arg Pro Asp Ser
      100                      105                      110                      115
```

```
ttc gtc ctg atc ctg gag agg ccc gag ccg gtg caa gat ctc ttc gac 681
Phe Val Leu Ile Leu Glu Arg Pro Glu Pro Val Gln Asp Leu Phe Asp
                      120                      125                      130
```

```
ttc atc acg gaa agg gga gcc ctg caa gag gag ctc gcc cgc agc ttc 729
Phe Ile Thr Glu Arg Gly Ala Leu Gln Glu Glu Leu Ala Arg Ser Phe
                      135                      140                      145
```

```
ttc tgg cag gtg ctg gag gcc gtg cgg cac tgc cac aac tgc ggg gtg 777
Phe Trp Gln Val Leu Glu Ala Val Arg His Cys His Asn Cys Gly Val
                      150                      155                      160
```

```
ctc cac cgc gac atc aag gac gaa aac atc ctt atc gac ctc aat cgc 825
Leu His Arg Asp Ile Lys Asp Glu Asn Ile Leu Ile Asp Leu Asn Arg
```



```

gaaaagcagt tctggatggg gtgccttcca gatcctctct ggggctgtgt tttgagcagc 2460
aggtagcctg gctgggtttta tctgagtga atactgtaca ggggaataaa agagatctta 2520
ttttt                                           2525

```

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<210> 18
<211> 313
<212> PRT
<213> Homo sapiens

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<400> 18

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Met Leu Leu Ser Lys Ile Asn Ser Leu Ala His Leu Arg Ala Ala Pro
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Cys Asn Asp Leu His Ala Thr Lys Leu Ala Pro Gly Lys Glu Lys Glu
 20          25          30
Pro Leu Glu Ser Gln Tyr Gln Val Gly Pro Leu Leu Gly Ser Gly Gly
 35          40          45
Phe Gly Ser Val Tyr Ser Gly Ile Arg Val Ser Asp Asn Leu Pro Val
 50          55          60
Ala Ile Lys His Val Glu Lys Asp Arg Ile Ser Asp Trp Gly Glu Leu
 65          70          75          80
Pro Asn Gly Thr Arg Val Pro Met Glu Val Val Leu Leu Lys Lys Val
 85          90          95
Ser Ser Gly Phe Ser Gly Val Ile Arg Leu Leu Asp Trp Phe Glu Arg
100          105          110
Pro Asp Ser Phe Val Leu Ile Leu Glu Arg Pro Glu Pro Val Gln Asp
115          120          125
Leu Phe Asp Phe Ile Thr Glu Arg Gly Ala Leu Gln Glu Glu Leu Ala
130          135          140
Arg Ser Phe Phe Trp Gln Val Leu Glu Ala Val Arg His Cys His Asn
145          150          155          160
Cys Gly Val Leu His Arg Asp Ile Lys Asp Glu Asn Ile Leu Ile Asp
165          170          175
Leu Asn Arg Gly Glu Leu Lys Leu Ile Asp Phe Gly Ser Gly Ala Leu
180          185          190
Leu Lys Asp Thr Val Tyr Thr Asp Phe Asp Gly Thr Arg Val Tyr Ser
195          200          205
Pro Pro Glu Trp Ile Arg Tyr His Arg Tyr His Gly Arg Ser Ala Ala
210          215          220
Val Trp Ser Leu Gly Ile Leu Leu Tyr Asp Met Val Cys Gly Asp Ile
225          230          235          240
Pro Phe Glu His Asp Glu Glu Ile Ile Arg Gly Gln Val Phe Phe Arg
245          250          255
Gln Arg Val Ser Ser Glu Cys Gln His Leu Ile Arg Trp Cys Leu Ala
260          265          270
Leu Arg Pro Ser Asp Arg Pro Thr Phe Glu Glu Ile Gln Asn His Pro
275          280          285
Trp Met Gln Asp Val Leu Leu Pro Gln Glu Thr Ala Glu Ile His Leu
290          295          300
His Ser Leu Ser Pro Gly Pro Ser Lys
305          310

```

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<210> 19
<211> 3401
<212> DNA
<213> Saccharomyces cerevisiae

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<220>
 <221> CDS
 <222> (789) ... (2795)

<400> 19

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tctatatattg	attaatctct	tgttatcttg	gtgatgatcg	cacaagtatg	tactcctgta	180
tctgcaagaa	tatctgtttt	aaacttttca	aagcaaggaa	accccgctctt	atatagggtta	240
tccgcaaagg	tcacattttc	ttgcaaatag	aagaaaaagc	accacaagc	acactaacac	300
agtgccagag	caaaactata	tcctttgcat	ccgatctcaa	acgctgttct	tatcgcatct	360
gtcttcgtcc	tttcatctgc	atttaccttt	tctttttcat	cctctatttg	ccttttcatt	420
agtggcaatt	tttccagttt	tttccctctg	cgtcccgttg	cacctgaaag	gatctttcta	480
acgtgtgttg	tctactagtg	agcgatttcg	tgagccatac	acgttctata	gaaaattgaa	540
taaactttac	ttcaaaggga	tctggacaca	gagataactg	cttacctgct	tgccggaaga	600
aaagaattac	taaaaaagaa	gacaagggta	gctgctattg	tgggtacacg	tttcacagaa	660
ctactttttc	cttgtccttc	tccagacatc	aacgtcatac	aactaaaact	gataaagtac	720
ccgtttttcc	gtacattttct	atagatacat	tattatatta	agcagatcga	gacgttaatt	780
tctcaaag	atg gaa gac	aag ttt gct	aac ctc agt	ctc cat gag	aaa act	830
	Met Glu Asp	Lys Phe Ala	Asn Leu Ser	Leu His Glu	Lys Thr	
	1	5	10			
ggg aag tca	tct atc caa	tta aac gag	caa aca ggc	tca gat aat	ggc	878
Gly Lys Ser	Ser Ser Ile	Gln Leu Asn	Glu Gln Thr	Gly Ser Asp	Asn Gly	
15	20	25	30			
tct gct gtc	aag aga aca	tct tcg acg	tcc tcg cac	tac aat aac	atc	926
Ser Ala Val	Lys Arg Thr	Ser Ser Thr	Ser Ser His	Tyr Asn Asn	Ile	
	35	40	45			
aac gct gac	ctt cat gct	cgt gta aaa	gct ttt caa	gaa caa cgt	gca	974
Asn Ala Asp	Leu His Ala	Arg Val Lys	Ala Phe Gln	Glu Gln Arg	Ala	
	50	55	60			
ttg aaa agg	tct gcc agc	gtg ggc agt	aat caa agc	gag caa gac	aaa	1022
Leu Lys Arg	Ser Ala Ser	Val Gly Ser	Asn Gln Ser	Glu Gln Asp	Lys	
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ggc agt tca	caa tca cct	aaa cat att	cag cag att	ggt aat aag	cca	1070
Gly Ser Ser	Gln Ser Pro	Lys His Ile	Gln Gln Ile	Val Asn Lys	Pro	
80	85	90				
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Leu Pro Pro	Leu Pro Val	Ala Gly Ser	Ser Ser Lys	Val Ser Gln	Arg Met	
95	100	105	110			
agt agc caa	gtc gtg caa	gcg tcc tcc	aag agc act	ctt aag aac	gtt	1166
Ser Ser Gln	Val Val Gln	Ala Ser Ser	Lys Ser Thr	Leu Lys Asn	Val	
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ctg gac aat	caa gaa aca	caa aac att	acc gac gta	aat att aac	atc	1214
Leu Asp Asn	Gln Glu Thr	Gln Asn Ile	Thr Asp Val	Asn Ile Asn	Ile	
	130	135	140			
gat aca acc	aaa att acc	gcc aca aca	att ggt gta	aat act ggc	cta	1262
Asp Thr Thr	Lys Ile Thr	Ala Thr Thr	Ile Gly Val	Asn Thr Gly	Leu	
145	150	155				

cct gct act gac att acg ccg tca gtt tct aat act gca tca gca aca	1310
Pro Ala Thr Asp Ile Thr Pro Ser Val Ser Asn Thr Ala Ser Ala Thr	
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cat aag gcg caa ttg ctg aat cct aac aga agg gca cca aga agg ccg	1358
His Lys Ala Gln Leu Leu Asn Pro Asn Arg Arg Ala Pro Arg Arg Pro	
175 180 185 190	
ctt tct acc cag cac cct aca aga cca aat gtt gcc ccg cat aag gcc	1406
Leu Ser Thr Gln His Pro Thr Arg Pro Asn Val Ala Pro His Lys Ala	
195 200 205	
cct gct ata atc aac aca cca aaa caa agt tta agt gcc cgt cga ggg	1454
Pro Ala Ile Ile Asn Thr Pro Lys Gln Ser Leu Ser Ala Arg Arg Gly	
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ctc aaa tta cca cca gga gga atg tca tta aaa atg ccc act aaa aca	1502
Leu Lys Leu Pro Pro Gly Gly Met Ser Leu Lys Met Pro Thr Lys Thr	
225 230 235	
gct caa cag ccg cag cag ttt gcc cca agc cct tca aac aaa aaa cat	1550
Ala Gln Gln Pro Gln Gln Phe Ala Pro Ser Pro Ser Asn Lys Lys His	
240 245 250	
ata gaa acc tta tca aac agc aaa gtt gtt gaa ggg aaa aga tcg aat	1598
Ile Glu Thr Leu Ser Asn Ser Lys Val Val Glu Gly Lys Arg Ser Asn	
255 260 265 270	
ccg ggt tct ttg ata aat ggt gtg caa agc aca tcc acc tca tca agt	1646
Pro Gly Ser Leu Ile Asn Gly Val Gln Ser Thr Ser Thr Ser Ser	
275 280 285	
acc gaa ggc cca cat gac act gta ggc act aca ccc aga act gga aac	1694
Thr Glu Gly Pro His Asp Thr Val Gly Thr Thr Pro Arg Thr Gly Asn	
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agc aac aac tct tca aat tct ggt agt agt ggt ggt ggt ggt ctt ttc	1742
Ser Asn Asn Ser Ser Asn Ser Gly Ser Ser Gly Gly Gly Gly Leu Phe	
305 310 315	
gca aat ttc tcg aaa tac gtg gat atc aaa tcc ggc tct ttg aat ttt	1790
Ala Asn Phe Ser Lys Tyr Val Asp Ile Lys Ser Gly Ser Leu Asn Phe	
320 325 330	
gca ggc aaa cta tcg cta tcc tct aaa gga ata gat ttc agc aat ggt	1838
Ala Gly Lys Leu Ser Leu Ser Ser Lys Gly Ile Asp Phe Ser Asn Gly	
335 340 345 350	
tct agt tcg aga att aca ttg gac gaa cta gaa ttt ttg gat gaa ctg	1886
Ser Ser Ser Arg Ile Thr Leu Asp Glu Leu Glu Phe Leu Asp Glu Leu	
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ggt cat ggt aac tat ggt aac gtc tca aag gta ctg cat aag ccc aca	1934
Gly His Gly Asn Tyr Gly Asn Val Ser Lys Val Leu His Lys Pro Thr	
370 375 380	

aat gtt att atg gcg acg aag gaa gtc cgt ttg gag cta gat gag gct	1982
Asn Val Ile Met Ala Thr Lys Glu Val Arg Leu Glu Leu Asp Glu Ala	
385 390 395	
aaa ttt aga caa att tta atg gaa cta gaa gtt ttg cat aaa tgc aat	2030
Lys Phe Arg Gln Ile Leu Met Glu Leu Glu Val Leu His Lys Cys Asn	
400 405 410	
tct ccc tat att gtg gat ttt tat ggt gca ttc ttt att gag ggc gcc	2078
Ser Pro Tyr Ile Val Asp Phe Tyr Gly Ala Phe Phe Ile Glu Gly Ala	
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gtc tac atg tgt atg gaa tac atg gat ggt ggt tcc ttg gat aaa ata	2126
Val Tyr Met Cys Met Glu Tyr Met Asp Gly Gly Ser Leu Asp Lys Ile	
435 440 445	
tac gac gaa tca tct gaa atc ggc ggc att gat gaa cct cag cta gcg	2174
Tyr Asp Glu Ser Ser Glu Ile Gly Gly Ile Asp Glu Pro Gln Leu Ala	
450 455 460	
ttt att gcc aat gct gtc att cat gga cta aaa gaa ctc aaa gag cag	2222
Phe Ile Ala Asn Ala Val Ile His Gly Leu Lys Glu Leu Lys Glu Gln	
465 470 475	
cat aat atc ata cac aga gat gtc aaa cca aca aat att tta tgt tca	2270
His Asn Ile Ile His Arg Asp Val Lys Pro Thr Asn Ile Leu Cys Ser	
480 485 490	
gcc aac caa ggc acc gta aag ctg tgc gat ttc ggt gtt tct ggt aat	2318
Ala Asn Gln Gly Thr Val Lys Leu Cys Asp Phe Gly Val Ser Gly Asn	
495 500 505 510	
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Leu Val Ala Ser Leu Ala Lys Thr Asn Ile Gly Cys Gln Ser Tyr Met	
515 520 525	
gca cct gaa cga atc aaa tcg ttg aat cca gat aga gcc acc tat acc	2414
Ala Pro Glu Arg Ile Lys Ser Leu Asn Pro Asp Arg Ala Thr Tyr Thr	
530 535 540	
gta cag tca gac atc tgg tct tta ggt tta agc att ctg gaa atg gca	2462
Val Gln Ser Asp Ile Trp Ser Leu Gly Leu Ser Ile Leu Glu Met Ala	
545 550 555	
cta ggt aga tat ccg tat cca cca gaa aca tac gac aac att ttc tct	2510
Leu Gly Arg Tyr Pro Tyr Pro Pro Glu Thr Tyr Asp Asn Ile Phe Ser	
560 565 570	
caa ttg agc gct att gtt gat ggg ccg cca ccg aga tta cct tca gat	2558
Gln Leu Ser Ala Ile Val Asp Gly Pro Pro Pro Arg Leu Pro Ser Asp	
575 580 585 590	
aaa ttc agt tct gac gca caa gat ttt gtt tct tta tgt cta caa aag	2606
Lys Phe Ser Ser Asp Ala Gln Asp Phe Val Ser Leu Cys Leu Gln Lys	
595 600 605	
att ccg gaa aga aga cct aca tac gca gct tta aca gag cat cct tgg	2654

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Leu	Pro	Pro	Gly	Gly	Met	Ser	Leu	Lys	Met	Pro	Thr	Lys	Thr	Ala	Gln
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Gln	Pro	Gln	Gln	Phe	Ala	Pro	Ser	Pro	Ser	Asn	Lys	Lys	His	Ile	Glu
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Thr	Leu	Ser	Asn	Ser	Lys	Val	Val	Glu	Gly	Lys	Arg	Ser	Asn	Pro	Gly
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Ser	Leu	Ile	Asn	Gly	Val	Gln	Ser	Thr	Ser	Thr	Ser	Ser	Ser	Thr	Glu
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Gly	Pro	His	Asp	Thr	Val	Gly	Thr	Thr	Pro	Arg	Thr	Gly	Asn	Ser	Asn
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Asn	Ser	Ser	Asn	Ser	Gly	Ser	Ser	Gly	Gly	Gly	Gly	Leu	Phe	Ala	Asn
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Phe	Ser	Lys	Tyr	Val	Asp	Ile	Lys	Ser	Gly	Ser	Leu	Asn	Phe	Ala	Gly
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Lys	Leu	Ser	Leu	Ser	Ser	Lys	Gly	Ile	Asp	Phe	Ser	Asn	Gly	Ser	Ser
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Ser	Arg	Ile	Thr	Leu	Asp	Glu	Leu	Glu	Phe	Leu	Asp	Glu	Leu	Gly	His
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Gly	Asn	Tyr	Gly	Asn	Val	Ser	Lys	Val	Leu	His	Lys	Pro	Thr	Asn	Val
	370					375					380				
Ile	Met	Ala	Thr	Lys	Glu	Val	Arg	Leu	Glu	Leu	Asp	Glu	Ala	Lys	Phe
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Arg	Gln	Ile	Leu	Met	Glu	Leu	Glu	Val	Leu	His	Lys	Cys	Asn	Ser	Pro
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Tyr	Ile	Val	Asp	Phe	Tyr	Gly	Ala	Phe	Phe	Ile	Glu	Gly	Ala	Val	Tyr
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Met	Cys	Met	Glu	Tyr	Met	Asp	Gly	Gly	Ser	Leu	Asp	Lys	Ile	Tyr	Asp
		435					440					445			
Glu	Ser	Ser	Glu	Ile	Gly	Gly	Ile	Asp	Glu	Pro	Gln	Leu	Ala	Phe	Ile
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Ala	Asn	Ala	Val	Ile	His	Gly	Leu	Lys	Glu	Leu	Lys	Glu	Gln	His	Asn
465					470					475					480
Ile	Ile	His	Arg	Asp	Val	Lys	Pro	Thr	Asn	Ile	Leu	Cys	Ser	Ala	Asn
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Gln	Gly	Thr	Val	Lys	Leu	Cys	Asp	Phe	Gly	Val	Ser	Gly	Asn	Leu	Val
			500					505					510		
Ala	Ser	Leu	Ala	Lys	Thr	Asn	Ile	Gly	Cys	Gln	Ser	Tyr	Met	Ala	Pro
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Glu	Arg	Ile	Lys	Ser	Leu	Asn	Pro	Asp	Arg	Ala	Thr	Tyr	Thr	Val	Gln
	530					535					540				
Ser	Asp	Ile	Trp	Ser											

cac agg gac ctg aag gtt tcc aac ttg ctc atg acc gac aag ggt tgt	648
His Arg Asp Leu Lys Val Ser Asn Leu Leu Met Thr Asp Lys Gly Cys	
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Val Lys Thr Ala Asp Phe Gly Leu Ala Arg Ala Tyr Gly Val Pro Val	
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aag cca atg acc ccc aag gtg gtc act ctc tgg tac cga gcc cct gaa	744
Lys Pro Met Thr Pro Lys Val Val Thr Leu Trp Tyr Arg Ala Pro Glu	
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Leu Leu Leu Gly Thr Thr Thr Gln Thr Thr Ser Ile Asp Met Trp Ala	
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Val Gly Cys Ile Leu Ala Glu Leu Leu Ala His Arg Pro Leu Leu Pro	
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Gly Thr Ser Glu Ile His Gln Ile Asp Leu Ile Val Gln Leu Leu Gly	
245 250 255	
acg ccc agt gag aac atc tgg ccg ggc ttt tcc aag ctg cca ctg gtc	936
Thr Pro Ser Glu Asn Ile Trp Pro Gly Phe Ser Lys Leu Pro Leu Val	
260 265 270	
ggc cag tac agc ctc cgg aag cag ccc tac aac aac ctg aag cac aag	984
Gly Gln Tyr Ser Leu Arg Lys Gln Pro Tyr Asn Asn Leu Lys His Lys	
275 280 285	
ttc cca tgg ctg tcg gag gcc ggg ctg cgc ctg ctg cac ttc ctg ttc	1032
Phe Pro Trp Leu Ser Glu Ala Gly Leu Arg Leu Leu His Phe Leu Phe	
290 295 300	
atg tac gac cct aag aaa agg gcg acg gcc ggg gac tgc ctg gag agc	1080
Met Tyr Asp Pro Lys Lys Arg Ala Thr Ala Gly Asp Cys Leu Glu Ser	
305 310 315 320	
tcc tat ttc aag gag aag ccc cta ccc tgt gag ccg gag ctc atg ccg	1128
Ser Tyr Phe Lys Glu Lys Pro Leu Pro Cys Glu Pro Glu Leu Met Pro	
325 330 335	
acc ttt ccc cac cac cgc aac aag cgg gcc gcc cca gcc acc tcc gag	1176
Thr Phe Pro His His Arg Asn Lys Arg Ala Ala Pro Ala Thr Ser Glu	
340 345 350	
ggc cag agc aag cgc tgt aaa ccc tga cggtgggcct ggcacacgcc	1223
Gly Gln Ser Lys Arg Cys Lys Pro *	
355 360	
tgtattccca caccaggtct tccgatcagt ggtgtctgtg aaggggtgccg cgagccaggc	1283
tgaccaggcg cccgggatcc agctcatccc cttggctggg aacatcctcc actgacttcc	1343
tcccactgtc tgccctgaac ccactgctgc ccccagaaaa aggccgggtg acaccggggg	1403
ctcccagccc gtgcaccctg gaagggcagg tctggcggct ccatccgtgg ctgcaggggt	1463
ctcatgtggg cctcctcgct atgttggaata tgtgcaacca ctgcttcttg ggaggagtgg	1523

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tgggtgcagt cccccgctg tctttgagtt gtggtggacc gctggcctgg gatgagaggg 1583
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gctggatccc tgctccccac acggaggacc caacaggagg ccgtggctct gatgctgagc 1823
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<210> 22
<211> 360
<212> PRT
<213> Homo sapiens

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Cys Arg Ser Val Lys Glu Phe Glu Lys Leu Asn Arg Ile Gly Glu Gly
          35          40          45
Thr Tyr Gly Ile Val Tyr Arg Ala Arg Asp Thr Gln Thr Asp Glu Ile
          50          55          60
Val Ala Leu Lys Lys Val Arg Met Asp Lys Glu Lys Asp Gly Ile Pro
65          70          75          80
Ile Ser Ser Leu Arg Glu Ile Thr Leu Leu Leu Arg Leu Arg His Pro
          85          90          95
Asn Ile Val Glu Leu Lys Glu Val Val Val Gly Asn His Leu Glu Ser
          100          105          110
Ile Phe Leu Val Met Gly Tyr Cys Glu Gln Asp Leu Ala Ser Leu Leu
          115          120          125
Glu Asn Met Pro Thr Pro Phe Ser Glu Ala Gln Val Lys Cys Ile Val
          130          135          140
Leu Gln Val Leu Arg Gly Leu Gln Tyr Leu His Arg Asn Phe Ile Ile
145          150          155          160
His Arg Asp Leu Lys Val Ser Asn Leu Leu Met Thr Asp Lys Gly Cys
          165          170          175
Val Lys Thr Ala Asp Phe Gly Leu Ala Arg Ala Tyr Gly Val Pro Val
          180          185          190
Lys Pro Met Thr Pro Lys Val Val Thr Leu Trp Tyr Arg Ala Pro Glu
          195          200          205
Leu Leu Leu Gly Thr Thr Thr Gln Thr Thr Ser Ile Asp Met Trp Ala
          210          215          220
Val Gly Cys Ile Leu Ala Glu Leu Leu Ala His Arg Pro Leu Leu Pro
225          230          235          240
Gly Thr Ser Glu Ile His Gln Ile Asp Leu Ile Val Gln Leu Leu Gly
          245          250          255
Thr Pro Ser Glu Asn Ile Trp Pro Gly Phe Ser Lys Leu Pro Leu Val
          260          265          270
Gly Gln Tyr Ser Leu Arg Lys Gln Pro Tyr Asn Asn Leu Lys His Lys
          275          280          285
Phe Pro Trp Leu Ser Glu Ala Gly Leu Arg Leu Leu His Phe Leu Phe
          290          295          300
Met Tyr Asp Pro Lys Lys Arg Ala Thr Ala Gly Asp Cys Leu Glu Ser
305          310          315          320
Ser Tyr Phe Lys Glu Lys Pro Leu Pro Cys Glu Pro Glu Leu Met Pro
          325          330          335
Thr Phe Pro His His Arg Asn Lys Arg Ala Ala Pro Ala Thr Ser Glu

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gaa gcc tat cag aag ctg tta aag agc ccg ccg aaa act gcc gga aca	651
Glu Ala Tyr Gln Lys Leu Leu Lys Ser Pro Pro Lys Thr Ala Gly Thr	
155 160 165 170	
tcc tct agc gtt gtc aca tct aca ttc agt ggc ttt tcc agc agc tcg	699
Ser Ser Ser Val Val Thr Ser Thr Phe Ser Gly Phe Ser Ser Ser Ser	
175 180 185	
tct atg aca agt aat ggt gtt tcc cag tca gca cct gga agt ttt tcc	747
Ser Met Thr Ser Asn Gly Val Ser Gln Ser Ala Pro Gly Ser Phe Ser	
190 195 200	
tca gag aac gtg ttt acg aac ggt ctc gga gaa aat aaa agg aaa tca	795
Ser Glu Asn Val Phe Thr Asn Gly Leu Gly Glu Asn Lys Arg Lys Ser	
205 210 215	
gga gta aaa gta tcc cct gat gat gtg caa aga aat aaa tat acc ttg	843
Gly Val Lys Val Ser Pro Asp Asp Val Gln Arg Asn Lys Tyr Thr Leu	
220 225 230	
gac gcc agg ttt aac agc gat ttt gaa gac ata gaa gaa att ggc tta	891
Asp Ala Arg Phe Asn Ser Asp Phe Glu Asp Ile Glu Glu Ile Gly Leu	
235 240 245 250	
ggt gga ttt ggt caa gtt ttc aaa gcg aaa cac aga att gat gga aag	939
Gly Gly Phe Gly Gln Val Phe Lys Ala Lys His Arg Ile Asp Gly Lys	
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aga tac gct att aag cgc gtt aaa tat aac acg gag aag gcg gag cac	987
Arg Tyr Ala Ile Lys Arg Val Lys Tyr Asn Thr Glu Lys Ala Glu His	
270 275 280	
gaa gta caa gcg ctg gca gaa ctc aat cac gtc aac att gtc caa tac	1035
Glu Val Gln Ala Leu Ala Glu Leu Asn His Val Asn Ile Val Gln Tyr	
285 290 295	
cat agt tgt tgg gag gga gtt gac tat gat cct gag cac agc atg agt	1083
His Ser Cys Trp Glu Gly Val Asp Tyr Asp Pro Glu His Ser Met Ser	
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Asp Thr Ser Arg Tyr Lys Thr Arg Cys Leu Phe Ile Gln Met Glu Phe	
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Cys Asp Lys Gly Thr Leu Glu Gln Trp Met Arg Asn Arg Asn Gln Ser	
335 340 345	
aaa gtg gac aaa gct ttg att ttg gac tta tat gaa caa atc gtg acc	1227
Lys Val Asp Lys Ala Leu Ile Leu Asp Leu Tyr Glu Gln Ile Val Thr	
350 355 360	
gga gtg gag tat ata cac tcg aaa ggg tta att cac aga gat ctt aag	1275
Gly Val Glu Tyr Ile His Ser Lys Gly Leu Ile His Arg Asp Leu Lys	
365 370 375	
cca ggt aat ata ttt tta gta gat gaa aga cac att aag atc gga gac	1323

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Pro Gly Asn Ile Phe Leu Val Asp Glu Arg His Ile Lys Ile Gly Asp
 380                               385                               390

ttt ggc ctt gca aca gcc ctg gaa aat gat gga aaa tcc cga aca agg 1371
Phe Gly Leu Ala Thr Ala Leu Glu Asn Asp Gly Lys Ser Arg Thr Arg
395                               400                               405                               410

aga aca gga act ctt caa tac atg agt cca gaa cag tta ttt tta aag 1419
Arg Thr Gly Thr Leu Gln Tyr Met Ser Pro Glu Gln Leu Phe Leu Lys
                               415                               420                               425

cac tat gga aaa gaa gtg gac atc ttt gct ttg ggc ctt att cta gct 1467
His Tyr Gly Lys Glu Val Asp Ile Phe Ala Leu Gly Leu Ile Leu Ala
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gaa ctt ctt cac acg tgc ttc acg gag tca gag aaa ata aag ttt ttc 1515
Glu Leu Leu His Thr Cys Phe Thr Glu Ser Glu Lys Ile Lys Phe Phe
                               445                               450                               455

gaa agt cta aga aaa ggc gac ttc tct aat gat ata ttc gac aac aaa 1563
Glu Ser Leu Arg Lys Gly Asp Phe Ser Asn Asp Ile Phe Asp Asn Lys
                               460                               465                               470

gaa aaa agc ctt cta aaa aaa cta ctc tca gag aaa ccc aag gac cga 1611
Glu Lys Ser Leu Leu Lys Lys Leu Leu Ser Glu Lys Pro Lys Asp Arg
475                               480                               485                               490

cct gag aca tct gaa atc ctg aag acc ttg gct gaa tgg agg aac atc 1659
Pro Glu Thr Ser Glu Ile Leu Lys Thr Leu Ala Glu Trp Arg Asn Ile
                               495                               500                               505

tca gag aaa gaa aag aaa cac atg tta ggg cct ttc tga gaaaacattc 1708
Ser Glu Lys Glu Lys Lys His Met Leu Gly Pro Phe *
                               510                               515

cttctgccgt ggttttcctt taacgatctg cagtctgagg ggagtatcag tgaatattat 1768
ccttcttttc ttaataccac tctcccagac aggttttggt tagggtgacc cacagacatt 1828
gtatttatta ggctatgaaa aagtatgccc atttcctcaa ttgttaattg ctgggcctgt 1888
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ttaagttagc tgggctacct gagagactgt cccagaaaac aggccaaaca ccttccttat 2248
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<211> 518
<212> PRT
<213> Mus musculus

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Gly Pro Pro His Asp Arg Arg Phe Thr Phe Gln Val Leu Ile Asp Glu

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Asp	Cys	His	Thr	Ser	Ala	Cys	Glu	Gln	Gly	Leu	Phe	Val	Gly	Asn	Tyr
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Ile	Gly	Leu	Val	Asn	Ser	Phe	Ala	Gln	Lys	Lys	Lys	Leu	Ser	Val	Asn
			100					105					110		
Tyr	Glu	Gln	Cys	Glu	Pro	Asn	Ser	Glu	Leu	Pro	Gln	Arg	Phe	Ile	Cys
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Leu	Lys	Ser	Pro	Pro	Lys	Thr	Ala	Gly	Thr	Ser	Ser	Ser	Val	Val	Thr
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Ser	Thr	Phe	Ser	Gly	Phe	Ser	Ser	Ser	Ser	Ser	Met	Thr	Ser	Asn	Gly
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Asp	Phe	Glu	Asp	Ile	Glu	Glu	Ile	Gly	Leu	Gly	Gly	Phe	Gly	Gln	Val
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Phe	Lys	Ala	Lys	His	Arg	Ile	Asp	Gly	Lys	Arg	Tyr	Ala	Ile	Lys	Arg
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Val	Lys	Tyr	Asn	Thr	Glu	Lys	Ala	Glu	His	Glu	Val	Gln	Ala	Leu	Ala
		275					280					285			
Glu	Leu	Asn	His	Val	Asn	Ile	Val	Gln	Tyr	His	Ser	Cys	Trp	Glu	Gly
	290					295					300				
Val	Asp	Tyr	Asp	Pro	Glu	His	Ser	Met	Ser	Asp	Thr	Ser	Arg	Tyr	Lys
305					310					315					320
Thr	Arg	Cys	Leu	Phe	Ile	Gln	Met	Glu	Phe	Cys	Asp	Lys	Gly	Thr	Leu
				325				330						335	
Glu	Gln	Trp	Met	Arg	Asn	Arg	Asn	Gln	Ser	Lys	Val	Asp	Lys	Ala	Leu
			340					345					350		
Ile	Leu	Asp	Leu	Tyr	Glu	Gln	Ile	Val	Thr	Gly	Val	Glu	Tyr	Ile	His
		355					360					365			
Ser	Lys	Gly	Leu	Ile	His	Arg	Asp	Leu	Lys	Pro	Gly	Asn	Ile	Phe	Leu
	370					375					380				
Val	Asp	Glu	Arg	His	Ile	Lys	Ile	Gly	Asp	Phe	Gly	Leu	Ala	Thr	Ala
385					390										

Leu Lys Thr Leu Ala Glu Trp Arg Asn Ile Ser Glu Lys Glu Lys Lys
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 His Met Leu Gly Pro Phe
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 tccctatcta ctttctctcc tcttgtagca agcctcagac tccaggcttg agctagggtt 180
 tgtttttctc ctggtgagaa ttcgaagacc atg tct acg gaa ctc ttc tca tcc 234
 Met Ser Thr Glu Leu Phe Ser Ser
 1 5

aca aga gag gaa gga agc tct ggc tca gga ccc agt ttt agg tct aat 282
 Thr Arg Glu Glu Gly Ser Ser Gly Ser Gly Pro Ser Phe Arg Ser Asn
 10 15 20

caa agg aaa atg tta aac ctg ctc ctg gag aga gac act tcc ttt acc 330
 Gln Arg Lys Met Leu Asn Leu Leu Leu Glu Arg Asp Thr Ser Phe Thr
 25 30 35 40

gtc tgt cca gat gtc cct aga act cca gtg ggc aaa ttt ctt ggt gat 378
 Val Cys Pro Asp Val Pro Arg Thr Pro Val Gly Lys Phe Leu Gly Asp
 45 50 55

tct gca aac cta agc att ttg tct gga gga acc cca aaa tgt tgc ctc 426
 Ser Ala Asn Leu Ser Ile Leu Ser Gly Gly Thr Pro Lys Cys Cys Leu
 60 65 70

gat ctt tcg aat ctt agc agt ggg gag ata act gcc act cag ctt acc 474
 Asp Leu Ser Asn Leu Ser Ser Gly Glu Ile Thr Ala Thr Gln Leu Thr
 75 80 85

act tct gca gac ctt gat gaa act ggt cac ctg gat tct tca gga ctt 522
 Thr Ser Ala Asp Leu Asp Glu Thr Gly His Leu Asp Ser Ser Gly Leu
 90 95 100

cag gaa gtg cat tta gct ggg atg aat cat gac cag cac cta atg aaa 570
 Gln Glu Val His Leu Ala Gly Met Asn His Asp Gln His Leu Met Lys
 105 110 115 120

tgt agc cca gca cag ctt ctt tgt agc act ccg aat ggt ttg gac cgt 618
 Cys Ser Pro Ala Gln Leu Leu Cys Ser Thr Pro Asn Gly Leu Asp Arg
 125 130 135

ggc cat aga aag aga gat gca atg tgt agt tca tct gca aat aaa gaa 666
 Gly His Arg Lys Arg Asp Ala Met Cys Ser Ser Ser Ala Asn Lys Glu

140	145	150	
aat gac aat gga aac ttg gtg gac agt gaa atg aaa tat ttg ggc agt Asn Asp Asn Gly Asn Leu Val Asp Ser Glu Met Lys Tyr Leu Gly Ser 155 160 165			714
ccc att act act gtt cca aaa ttg gat aaa aat cca aac cta gga gaa Pro Ile Thr Thr Val Pro Lys Leu Asp Lys Asn Pro Asn Leu Gly Glu 170 175 180			762
gac cag gca gaa gag att tca gat gaa tta atg gag ttt tcc ctg aaa Asp Gln Ala Glu Glu Ile Ser Asp Glu Leu Met Glu Phe Ser Leu Lys 185 190 195 200			810
gat caa gaa gca aag gtg agc aga agt ggc cta tat cgc tcc ccg tcg Asp Gln Glu Ala Lys Val Ser Arg Ser Gly Leu Tyr Arg Ser Pro Ser 205 210 215			858
atg cca gag aac ttg aac agg cca aga ctg aag cag gtg gaa aaa ttc Met Pro Glu Asn Leu Asn Arg Pro Arg Leu Lys Gln Val Glu Lys Phe 220 225 230			906
aag gac aac aca ata cca gat aaa gtt aaa aaa aag tat ttt tct ggc Lys Asp Asn Thr Ile Pro Asp Lys Val Lys Lys Lys Tyr Phe Ser Gly 235 240 245			954
caa gga aag ctc agg aag ggc tta tgt tta aag aag aca gtc tct ctg Gln Gly Lys Leu Arg Lys Gly Leu Cys Leu Lys Lys Thr Val Ser Leu 250 255 260			1002
tgt gac att act atc act cag atg ctg gag gaa gat tct aac cag ggg Cys Asp Ile Thr Ile Thr Gln Met Leu Glu Glu Asp Ser Asn Gln Gly 265 270 275 280			1050
cac ctg att ggt gat ttt tcc aag gta tgt gcg ctg cca acc gtg tca His Leu Ile Gly Asp Phe Ser Lys Val Cys Ala Leu Pro Thr Val Ser 285 290 295			1098
ggg aaa cac caa gat ctg aag tat gtc aac cca gaa aca gtg gct gcc Gly Lys His Gln Asp Leu Lys Tyr Val Asn Pro Glu Thr Val Ala Ala 300 305 310			1146
tta ctg tcg ggg aag ttc cag ggt ctg att gag aag ttt tat gtc att Leu Leu Ser Gly Lys Phe Gln Gly Leu Ile Glu Lys Phe Tyr Val Ile 315 320 325			1194
gat tgt cgc tat cca tat gag tat ctg gga gga cac atc cag gga gcc Asp Cys Arg Tyr Pro Tyr Glu Tyr Leu Gly Gly His Ile Gln Gly Ala 330 335 340			1242
tta aac tta tat agt cag gaa gaa ctg ttt aac ttc ttt ctg aag aag Leu Asn Leu Tyr Ser Gln Glu Glu Leu Phe Asn Phe Phe Leu Lys Lys 345 350 355 360			1290
ccc atc gtc cct ttg gac acc cag aag aga ata atc atc gtg ttc cac Pro Ile Val Pro Leu Asp Thr Gln Lys Arg Ile Ile Ile Val Phe His 365 370 375			1338

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<210> 29
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 Asn Thr Arg Gln Phe Ser Asp Asp Glu Glu Phe Thr Thr Pro Pro Lys
 20 25 30
 cta agc aat ttc gga tca gct tta ctt tcc cac aca gaa aaa act tca 144
 Leu Ser Asn Phe Gly Ser Ala Leu Leu Ser His Thr Glu Lys Thr Ser
 35 40 45
 gca tca gag ata tta tca agt cat aat aat gac aag atc gca aat cga 192
 Ala Ser Glu Ile Leu Ser Ser His Asn Asn Asp Lys Ile Ala Asn Arg
 50 55 60
 tta gaa gaa atg gac agg agt tca tca agg agt cac ccc cca ccg tca 240
 Leu Glu Glu Met Asp Arg Ser Ser Ser Arg Ser His Pro Pro Pro Ser
 65 70 75 80
 atg ggc aat ttg aca tcc ggt cat act agt acc tca tcg cat tca acc 288
 Met Gly Asn Leu Thr Ser Gly His Thr Ser Thr Ser Ser His Ser Thr
 85 90 95
 ttg ttc gga cga tat ctg aga aat aat cac cag act agc atg acg acg 336
 Leu Phe Gly Arg Tyr Leu Arg Asn Asn His Gln Thr Ser Met Thr Thr
 100 105 110
 atg aac act agt gac ata gag ata aat gtt gga aat agt ctt gat aag 384
 Met Asn Thr Ser Asp Ile Glu Ile Asn Val Gly Asn Ser Leu Asp Lys
 115 120 125
 agt ttt gaa agg ata agg aat ttg cga caa aat atg aaa gaa gat att 432
 Ser Phe Glu Arg Ile Arg Asn Leu Arg Gln Asn Met Lys Glu Asp Ile

130	135	140	
acg gca aag tat gct gaa agg aga agt aag aga ttt tta ata tcc aat			480
Thr Ala Lys Tyr Ala Glu Arg Arg Ser Lys Arg Phe Leu Ile Ser Asn			
145	150	155	160
agg aca acg aag ctg ggt cct gca aag aga gcg atg act ttg aca aat			528
Arg Thr Thr Lys Leu Gly Pro Ala Lys Arg Ala Met Thr Leu Thr Asn			
	165	170	175
atc ttt gat gag gat gtg cct aac tct cca aac cag cca ata aat gca			576
Ile Phe Asp Glu Asp Val Pro Asn Ser Pro Asn Gln Pro Ile Asn Ala			
	180	185	190
agg gag aca gtg gaa tta cca ctt gag gat tct cac caa aca aac ttt			624
Arg Glu Thr Val Glu Leu Pro Leu Glu Asp Ser His Gln Thr Asn Phe			
	195	200	205
aaa gaa cga aga gag aat acg gat tat gat tca att gat ttt gga gat			672
Lys Glu Arg Arg Glu Asn Thr Asp Tyr Asp Ser Ile Asp Phe Gly Asp			
	210	215	220
ttg aat cct atc cag tat att aaa aaa cat aat ctt ccc aca agt gac			720
Leu Asn Pro Ile Gln Tyr Ile Lys Lys His Asn Leu Pro Thr Ser Asp			
	225	230	240
ctt cca cta ata tct caa atc tac ttt gat aaa caa aga gaa gaa aat			768
Leu Pro Leu Ile Ser Gln Ile Tyr Phe Asp Lys Gln Arg Glu Glu Asn			
	245	250	255
aga caa gca gca ctc cga aaa cat agt tcc aga gaa ttg ctt tat aaa			816
Arg Gln Ala Ala Leu Arg Lys His Ser Ser Arg Glu Leu Leu Tyr Lys			
	260	265	270
agt agg tct tct tcc tct tca ctt tct agt aac aac tta ttg gca aac			864
Ser Arg Ser Ser Ser Ser Ser Leu Ser Ser Asn Asn Leu Leu Ala Asn			
	275	280	285
aag gac aat tct ata aca tcc aat aat ggt tct caa ccc agg cga aaa			912
Lys Asp Asn Ser Ile Thr Ser Asn Asn Gly Ser Gln Pro Arg Arg Lys			
	290	295	300
gtt tct act gga tca tct tca tct aag tca tcg atc gaa ata aga aga			960
Val Ser Thr Gly Ser Ser Ser Ser Lys Ser Ser Ile Glu Ile Arg Arg			
	305	310	320
gct ctc aag gag aat att gat act agc aat aac agc aat ttc aac agc			1008
Ala Leu Lys Glu Asn Ile Asp Thr Ser Asn Asn Ser Asn Phe Asn Ser			
	325	330	335
cca att cat aaa att tat aaa gga att tcc aga aat aaa gat tcc gac			1056
Pro Ile His Lys Ile Tyr Lys Gly Ile Ser Arg Asn Lys Asp Ser Asp			
	340	345	350
tcc gaa aaa aga gaa gta ctg cga aac ata agc ata aat gca aat cac			1104
Ser Glu Lys Arg Glu Val Leu Arg Asn Ile Ser Ile Asn Ala Asn His			
	355	360	365

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Asn	Ile	Tyr	Arg	Glu	Thr	Gln	Ile	Gly	Thr	Pro	Asn	Tyr	Met	Ala	Pro	
		595					600					605				
gaa	gca	cta	gtt	gct	atg	aat	tac	aca	caa	aat	agt	gag	aac	caa	cat	1872
Glu	Ala	Leu	Val	Ala	Met	Asn	Tyr	Thr	Gln	Asn	Ser	Glu	Asn	Gln	His	
	610					615					620					
gag	gga	aac	aag	tgg	aaa	gtg	ggg	aga	cca	tct	gat	atg	tgg	tca	tgc	1920
Glu	Gly	Asn	Lys	Trp	Lys	Val	Gly	Arg	Pro	Ser	Asp	Met	Trp	Ser	Cys	
625					630					635					640	
ggg	tgt	att	ata	tat	cag	atg	att	tac	ggg	aaa	ccc	cca	tat	ggc	agt	1968
Gly	Cys	Ile	Ile	Tyr	Gln	Met	Ile	Tyr	Gly	Lys	Pro	Pro	Tyr	Gly	Ser	
				645					650					655		
ttc	caa	ggc	caa	aat	agg	ctg	ttg	gct	att	atg	aat	cct	gat	gtg	aaa	2016
Phe	Gln	Gly	Gln	Asn	Arg	Leu	Leu	Ala	Ile	Met	Asn	Pro	Asp	Val	Lys	
			660					665					670			
atc	cca	ttt	cct	gaa	cat	act	agc	aat	aat	gaa	aag	att	cca	aag	tct	2064
Ile	Pro	Phe	Pro	Glu	His	Thr	Ser	Asn	Asn	Glu	Lys	Ile	Pro	Lys	Ser	
		675					680					685				
gcc	att	gaa	tta	atg	aaa	gca	tgt	ctg	tac	agg	aac	cca	gac	aaa	aga	2112
Ala	Ile	Glu	Leu	Met	Lys	Ala	Cys	Leu	Tyr	Arg	Asn	Pro	Asp	Lys	Arg	
	690					695					700					
tgg	act	gtg	gat	aaa	gtc	ctg	agt	agc	act	ttc	ctt	caa	cct	ttt	atg	2160
Trp	Thr	Val	Asp	Lys	Val	Leu	Ser	Ser	Thr	Phe	Leu	Gln	Pro	Phe	Met	
705					710					715					720	
ata	tcc	gga	tcg	att	atg	gaa	gac	ctt	att	agg	aat	gcc	gtt	aga	tat	2208
Ile	Ser	Gly	Ser	Ile	Met	Glu	Asp	Leu	Ile	Arg	Asn	Ala	Val	Arg	Tyr	
				725					730					735		
ggc	tct	gag	aag	cct	cat	ata	tca	caa	gat	gat	ctc	aat	gat	gtg	gta	2256
Gly	Ser	Glu	Lys	Pro	His	Ile	Ser	Gln	Asp	Asp	Leu	Asn	Asp	Val	Val	
			740					745					750			
gac	act	gtt	tta	agg	aaa	ttt	gca	gat	tac	aaa	att	tag				2295
Asp	Thr	Val	Leu	Arg	Lys	Phe	Ala	Asp	Tyr	Lys	Ile	*				
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<211> 764

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 30

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			20					25					30		
Leu	Ser	Asn	Phe	Gly	Ser	Ala	Leu	Leu	Ser	His	Thr	Glu	Lys	Thr	Ser
		35					40					45			

Ala	Ser	Glu	Ile	Leu	Ser	Ser	His	Asn	Asn	Asp	Lys	Ile	Ala	Asn	Arg
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Leu	Glu	Glu	Met	Asp	Arg	Ser	Ser	Ser	Arg	Ser	His	Pro	Pro	Pro	Ser
65					70					75					80
Met	Gly	Asn	Leu	Thr	Ser	Gly	His	Thr	Ser	Thr	Ser	Ser	His	Ser	Thr
				85					90					95	
Leu	Phe	Gly	Arg	Tyr	Leu	Arg	Asn	Asn	His	Gln	Thr	Ser	Met	Thr	Thr
			100					105					110		
Met	Asn	Thr	Ser	Asp	Ile	Glu	Ile	Asn	Val	Gly	Asn	Ser	Leu	Asp	Lys
		115					120					125			
Ser	Phe	Glu	Arg	Ile	Arg	Asn	Leu	Arg	Gln	Asn	Met	Lys	Glu	Asp	Ile
	130					135					140				
Thr	Ala	Lys	Tyr	Ala	Glu	Arg	Arg	Ser	Lys	Arg	Phe	Leu	Ile	Ser	Asn
145					150					155					160
Arg	Thr	Thr	Lys	Leu	Gly	Pro	Ala	Lys	Arg	Ala	Met	Thr	Leu	Thr	Asn
				165					170					175	
Ile	Phe	Asp	Glu	Asp	Val	Pro	Asn	Ser	Pro	Asn	Gln	Pro	Ile	Asn	Ala
			180					185					190		
Arg	Glu	Thr	Val	Glu	Leu	Pro	Leu	Glu	Asp	Ser	His	Gln	Thr	Asn	Phe
		195					200					205			
Lys	Glu	Arg	Arg	Glu	Asn	Thr	Asp	Tyr	Asp	Ser	Ile	Asp	Phe	Gly	Asp
	210					215					220				
Leu	Asn	Pro	Ile	Gln	Tyr	Ile	Lys	Lys	His	Asn	Leu	Pro	Thr	Ser	Asp
225					230					235					240
Leu	Pro	Leu	Ile	Ser	Gln	Ile	Tyr	Phe	Asp	Lys	Gln	Arg	Glu	Glu	Asn
				245					250					255	
Arg	Gln	Ala	Ala	Leu	Arg	Lys	His	Ser	Ser	Arg	Glu	Leu	Leu	Tyr	Lys
			260					265					270		
Ser	Arg	Ser	Ser	Ser	Ser	Ser	Leu	Ser	Ser	Asn	Asn	Leu	Leu	Ala	Asn
		275					280					285			
Lys	Asp	Asn	Ser	Ile	Thr	Ser	Asn	Asn	Gly	Ser	Gln	Pro	Arg	Arg	Lys
	290					295					300				
Val	Ser	Thr	Gly	Ser	Ser	Ser	Ser	Lys	Ser	Ser	Ile	Glu	Ile	Arg	Arg
305					310					315					320
Ala	Leu	Lys	Glu	Asn	Ile	Asp	Thr	Ser	Asn	Asn	Ser	Asn	Phe	Asn	Ser
				325					330					335	
Pro	Ile	His	Lys	Ile	Tyr	Lys	Gly	Ile	Ser	Arg	Asn	Lys	Asp	Ser	Asp
			340					345					350		
Ser	Glu	Lys	Arg	Glu	Val	Leu	Arg	Asn	Ile	Ser	Ile	Asn	Ala	Asn	His
		355					360					365			
Ala	Asp	Asn	Leu	Leu	Gln	Gln	Glu	Asn	Lys	Arg	Leu	Lys	Arg	Ser	Leu
	370					375					380				
Asp	Asp	Ala	Ile	Thr	Asn	Glu	Asn	Ile	Asn	Ser	Lys	Asn	Leu	Glu	Val
385					390					395					400
Phe	Tyr	His</													

gac	act	ttc	tct	tcc	aag	agt	agc	cat	tct	gat	ggc	acc	gtt	act	ggg	197
Asp	Thr	Phe	Ser	Ser	Lys	Ser	Ser	His	Ser	Asp	Gly	Thr	Val	Thr	Gly	
				45					50					55		
gat	acg	ttg	cgt	agg	cag	tca	agc	ggg	gca	act	gct	tta	gag	aga	ttg	245
Asp	Thr	Leu	Arg	Arg	Gln	Ser	Ser	Gly	Ala	Thr	Ala	Leu	Glu	Arg	Leu	
			60					65					70			
gtc	tca	cat	cct	cgt	act	aaa	aat	ttt	gat	ttg	caa	gga	aat	gga	gga	293
Val	Ser	His	Pro	Arg	Thr	Lys	Asn	Phe	Asp	Leu	Gln	Gly	Asn	Gly	Gly	
		75					80					85				
caa	aat	tct	gct	ttg	aag	gaa	gtg	aat	act	cca	gca	tat	cag	tca	atg	341
Gln	Asn	Ser	Ala	Leu	Lys	Glu	Val	Asn	Thr	Pro	Ala	Tyr	Gln	Ser	Met	
	90					95					100					
cac	cat	ttc	gag	cat	tta	ata	aca	ccc	ttg	ccc	tct	act	aat	gcg	tct	389
His	His	Phe	Glu	His	Leu	Ile	Thr	Pro	Leu	Pro	Ser	Thr	Asn	Ala	Ser	
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His	Ser	Glu	Val	Ser	Leu	Ser	Ala	Gly	Val	Asn	Asp	Leu	Asn	Ser	Asn	
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tcg	gag	cat	gat	ttg	tta	cct	aaa	agt	gta	aac	aaa	acc	ccc	ggg	tct	485
Ser	Glu	His	Asp	Leu	Leu	Pro	Lys	Ser	Val	Asn	Lys	Thr	Pro	Gly	Ser	
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tta	tca	att	tca	aga	cga	cga	aga	atc	ggc	aga	att	gga	tta	ggc	cct	533
Leu	Ser	Ile	Ser	Arg	Arg	Arg	Arg	Ile	Gly	Arg	Ile	Gly	Leu	Gly	Pro	
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cca	aag	cgt	gct	gag	tac	acg	ttg	acg	gat	ccc	tcg	aag	act	tcc	gat	581
Pro	Lys	Arg	Ala	Glu	Tyr	Thr	Leu	Thr	Asp	Pro	Ser	Lys	Thr	Ser	Asp	
	170					175					180					
acc	aaa	aac	tct	aca	gaa	gca	gat	gag	gat	att	gaa	atg	aaa	tct	cga	629
Thr	Lys	Asn	Ser	Thr	Glu	Ala	Asp	Glu	Asp	Ile	Glu	Met	Lys	Ser	Arg	
185					190					195					200	
gaa	gta	tca	cca	gct	tcc	aac	tct	gtt	gct	gca	aca	act	tta	aaa	cct	677
Glu	Val	Ser	Pro	Ala	Ser	Asn	Ser	Val	Ala	Ala	Thr	Thr	Leu	Lys	Pro	
				205					210					215		
ctg	cag	ctg	cat	aac	act	cct	ttg	caa	aca	tcc	cag	gag	cat	ccc	aaa	725
Leu	Gln	Leu	His	Asn	Thr	Pro	Leu	Gln	Thr	Ser	Gln	Glu	His	Pro	Lys	
			220					225					230			
cct	tct	ttt	cat	cct	tct	cag	ttt	gag	agc	tct	ttt	tct	cct	agg	gtg	773
Pro	Ser	Phe	His	Pro	Ser	Gln	Phe	Glu	Ser	Ser	Phe	Ser	Pro	Arg	Val	
		235					240					245				
cag	ttt	gat	cac	gat	gtt	gaa	aga	aga	gct	agt	gaa	ctt	cat	tct	cgt	821
Gln	Phe	Asp	His	Asp	Val	Glu	Arg	Arg	Ala	Ser	Glu	Leu	His	Ser	Arg	
	250					255					260					
cca	gtc	acc	gtt	ttc	caa	gag	cct	cag	cgt	tct	gct	tct	caa	cca	tat	869

Pro	Val	Thr	Val	Phe	Gln	Glu	Pro	Gln	Arg	Ser	Ala	Ser	Gln	Pro	Tyr	
265					270					275					280	
gaa	tct	cat	gct	ctt	tct	cca	aag	gtg	gct	ccg	tta	ttt	gat	aac	agt	917
Glu	Ser	His	Ala	Leu	Ser	Pro	Lys	Val	Ala	Pro	Leu	Phe	Asp	Asn	Ser	
				285					290					295		
caa	gct	act	ccc	ata	ccc	aag	cgt	cag	cag	gac	gtt	gtt	act	gtt	gcc	965
Gln	Ala	Thr	Pro	Ile	Pro	Lys	Arg	Gln	Gln	Asp	Val	Val	Thr	Val	Ala	
			300					305					310			
aat	cta	caa	ttt	atc	aaa	tta	gga	gtt	gtt	gga	aag	ggg	gga	agt	agt	1013
Asn	Leu	Gln	Phe	Ile	Lys	Leu	Gly	Val	Val	Gly	Lys	Gly	Gly	Ser	Ser	
		315					320					325				
atg	gta	tat	cgc	ata	ttt	tcc	ccc	gat	aac	agt	cgt	tta	tac	gct	ttg	1061
Met	Val	Tyr	Arg	Ile	Phe	Ser	Pro	Asp	Asn	Ser	Arg	Leu	Tyr	Ala	Leu	
	330					335					340					
aaa	gag	gtg	aac	ttt	att	aat	gca	gac	caa	act	act	ata	caa	gga	tac	1109
Lys	Glu	Val	Asn	Phe	Ile	Asn	Ala	Asp	Gln	Thr	Thr	Ile	Gln	Gly	Tyr	
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aag	aac	gaa	att	gca	tta	tta	aga	aag	ctt	tca	ggc	aat	gat	cgc	ata	1157
Lys	Asn	Glu	Ile	Ala	Leu	Leu	Arg	Lys	Leu	Ser	Gly	Asn	Asp	Arg	Ile	
				365					370					375		
att	aaa	tta	tat	gct	gcc	gaa	gtt	aat	gat	act	tta	ggg	caa	ctc	aat	1205
Ile	Lys	Leu	Tyr	Ala	Ala	Glu	Val	Asn	Asp	Thr	Leu	Gly	Gln	Leu	Asn	
			380					385					390			
atg	gtg	atg	gaa	tgc	gga	gaa	acg	gat	tta	gca	aac	ctt	tta	atg	aaa	1253
Met	Val	Met	Glu	Cys	Gly	Glu	Thr	Asp	Leu	Ala	Asn	Leu	Leu	Met	Lys	
		395					400					405				
aac	atg	aag	aaa	ccc	att	aat	ctt	aat	ttc	atc	aga	atg	tat	tgg	gag	1301
Asn	Met	Lys	Lys	Pro	Ile	Asn	Leu	Asn	Phe	Ile	Arg	Met	Tyr	Trp	Glu	
	410					415					420					
caa	atg	cta	gag	gcg	gtc	cag	gta	gtt	cat	gat	caa	aat	ata	gtg	cat	1349
Gln	Met	Leu	Glu	Ala	Val	Gln	Val	Val	His	Asp	Gln	Asn	Ile	Val	His	
425					430					435					440	
tcg	gat	ttg	aag	ccg	gcc	aat	ttc	ctg	ctt	gta	gaa	ggg	aat	ttg	aag	1397
Ser	Asp	Leu	Lys	Pro	Ala	Asn	Phe	Leu	Leu	Val	Glu	Gly	Asn	Leu	Lys	
				445					450					455		
ctg	att	gat	ttt	ggc	att	gcc	aaa	gca	att	ggg	aat	gac	acc	act	aat	1445
Leu	Ile	Asp	Phe	Gly	Ile	Ala	Lys	Ala	Ile	Gly	Asn	Asp	Thr	Thr	Asn	
			460					465					470			
atc	cat	cgt	gat	tcc	cac	atc	ggg	act	att	aat	tat	atg	gca	cct	gaa	1493
Ile	His	Arg	Asp	Ser	His	Ile	Gly	Thr	Ile	Asn	Tyr	Met	Ala	Pro	Glu	
		475					480					485				
gct	ttg	aca	gac	atg	aat	gct	cac	aca	aac	tct	ggc	gtg	aaa	ctc	gta	1541
Ala	Leu	Thr	Asp	Met	Asn	Ala	His	Thr	Asn	Ser	Gly	Val	Lys	Leu	Val	

			20					25				30				
Asp	Pro	Glu	Leu	Tyr	Phe	Lys	Asn	Asp	Thr	Phe	Ser	Ser	Lys	Ser	Ser	
		35					40					45				
His	Ser	Asp	Gly	Thr	Val	Thr	Gly	Asp	Thr	Leu	Arg	Arg	Gln	Ser	Ser	
	50					55					60					
Gly	Ala	Thr	Ala	Leu	Glu	Arg	Leu	Val	Ser	His	Pro	Arg	Thr	Lys	Asn	
65					70					75					80	
Phe	Asp	Leu	Gln	Gly	Asn	Gly	Gly	Gln	Asn	Ser	Ala	Leu	Lys	Glu	Val	
			85					90					95			
Asn	Thr	Pro	Ala	Tyr	Gln	Ser	Met	His	His	Phe	Glu	His	Leu	Ile	Thr	
		100						105					110			
Pro	Leu	Pro	Ser	Thr	Asn	Ala	Ser	His	Ser	Glu	Val	Ser	Leu	Ser	Ala	
	115						120					125				
Gly	Val	Asn	Asp	Leu	Asn	Ser	Asn	Ser	Glu	His	Asp	Leu	Leu	Pro	Lys	
	130				135						140					
Ser	Val	Asn	Lys	Thr	Pro	Gly	Ser	Leu	Ser	Ile	Ser	Arg	Arg	Arg	Arg	
145					150					155					160	
Ile	Gly	Arg	Ile	Gly	Leu	Gly	Pro	Pro	Lys	Arg	Ala	Glu	Tyr	Thr	Leu	
			165						170					175		
Thr	Asp	Pro	Ser	Lys	Thr	Ser	Asp	Thr	Lys	Asn	Ser	Thr	Glu	Ala	Asp	
		180						185					190			
Glu	Asp	Ile	Glu	Met	Lys	Ser	Arg	Glu	Val	Ser	Pro	Ala	Ser	Asn	Ser	
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Val	Ala	Ala	Thr	Thr	Leu	Lys	Pro	Leu	Gln	Leu	His	Asn	Thr	Pro	Leu	
	210					215					220					
Gln	Thr	Ser	Gln	Glu	His	Pro	Lys	Pro	Ser	Phe	His	Pro	Ser	Gln	Phe	
225					230					235					240	
Glu	Ser	Ser	Phe	Ser	Pro	Arg	Val	Gln	Phe	Asp	His	Asp	Val	Glu	Arg	
			245						250					255		
Arg	Ala	Ser	Glu	Leu	His	Ser	Arg	Pro	Val	Thr	Val	Phe	Gln	Glu	Pro	
		260						265					270			
Gln	Arg	Ser	Ala	Ser	Gln	Pro	Tyr	Glu	Ser	His	Ala	Leu	Ser	Pro	Lys	
	275						280					285				
Val	Ala	Pro	Leu	Phe	Asp	Asn	Ser	Gln	Ala	Thr	Pro	Ile	Pro	Lys	Arg	
	290				295						300					
Gln	Gln	Asp	Val	Val	Thr	Val	Ala	Asn	Leu	Gln	Phe	Ile	Lys	Leu	Gly	
305					310					315					320	
Val	Val	Gly	Lys	Gly	Gly	Ser	Ser	Met	Val	Tyr	Arg	Ile	Phe	Ser	Pro	
			325						330				335			
Asp	Asn	Ser	Arg	Leu	Tyr	Ala	Leu	Lys	Glu	Val	Asn	Phe	Ile	Asn	Ala	
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Asp	Gln	Thr	Thr	Ile	Gln	Gly	Tyr	Lys	Asn	Glu	Ile	Ala	Leu	Leu	Arg	
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Lys	Leu	Ser	Gly	Asn	Asp	Arg	Ile	Ile	Lys	Leu	Tyr	Ala	Ala	Glu	Val	
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Asn	Asp	Thr	Leu	Gly	Gln	Leu	Asn	Met	Val	Met	Glu	Cys	Gly	Glu	Thr	
385					390					395					400	
Asp	Leu	Ala	Asn	Leu	Leu	Met	Lys	Asn	Met	Lys	Lys	Pro	Ile	Asn	Leu	
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Asn	Phe	Ile	Arg	Met	Tyr	Trp	Glu	Gln	Met	Leu	Glu	Ala	Val	Gln	Val	
		420						425					430			
Val	His	Asp	Gln	Asn	Ile	Val	His	Ser	Asp	Leu	Lys	Pro	Ala	Asn	Phe	
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Leu	Leu	Val	Glu	Gly	Asn	Leu	Lys	Leu	Ile	Asp	Phe	Gly	Ile	Ala	Lys	
	450				455					460						
Ala	Ile	Gly	Asn	Asp	Thr	Thr	Asn	Ile	His	Arg	Asp	Ser	His	Ile	Gly	
465					470					475					480	

Thr Ile Asn Tyr Met Ala Pro Glu Ala Leu Thr Asp Met Asn Ala His
485 490 495
Thr Asn Ser Gly Val Lys Leu Val Lys Leu Gly Arg Pro Ser Asp Val
500 505 510
Trp Ser Leu Gly Cys Ile Leu Tyr Gln Met Val Tyr Gly Arg Ala Pro
515 520 525
Phe Ala His Leu Lys Met Ile Gln Ala Ile Ala Ala Ile Pro Asn Glu
530 535 540
Gln Tyr His Ile His Phe Pro Glu Val Ala Leu Pro Ala Asn Ala Val
545 550 555 560
Gln Glu Lys Glu Gly Ser Leu Pro Gly Val Thr Val Gly Pro Asp Leu
565 570 575
Met Asp Val Met Lys Arg Cys Leu Glu Arg Asp Gln Arg Lys Arg Leu
580 585 590
Thr Ile Pro Glu Leu Leu Val His Pro Phe Leu Asn Pro Leu Pro Ser
595 600 605
Tyr Leu Thr Pro Leu Ala Lys Lys Pro Leu Pro Val Ser Gly His Thr
610 615 620
Asn Asn Ala His Pro Leu Arg Leu Ser Thr Glu Ile Ser Ala Ser Gln
625 630 635 640
Leu Ser Met Ile Ile Glu Arg Ser Val Glu Leu Ser Lys His Lys Arg
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660 665 670
Leu Arg Lys Met Pro Glu
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gccgccccgc ggtccccaga gcgccaggcc cccgggggga gggaggagg gcgccgggccc 180
ggtgggagcc agcggcgcgc ggtgggaccc acggagcccc gcgacccgcc gagcctggag 240
ccgggcccgc tcggggaagc cggctccagc ccggagcgaa ctctgcagcc cgtcgggggg 300
cggcgggggag ggggcccggg gccggaggag ggggcggccg cgggcacccc cgctgtgcc 360
ccggcggtccc cgggcacc atg ctg tcc aac tcc cag ggc cag agc ccg ccg 411
Met Leu Ser Asn Ser Gln Gly Gln Ser Pro Pro
1 5 10
gtg ccg ttc ccc gcc ccg gcc ccg ccg ccg cag ccc ccc acc cct gcc 459
Val Pro Phe Pro Ala Pro Ala Pro Pro Pro Gln Pro Pro Thr Pro Ala
15 20 25
ctg ccg cac ccc ccg gcg cag ccg ccg ccg ccg ccc ccg cag cag ttc 507
Leu Pro His Pro Pro Ala Gln Pro Pro Pro Pro Pro Pro Gln Gln Phe
30 35 40
ccg cag ttc cac gtc aag tcc ggc ctg cag atc aag aag aac gcc atc 555

Pro	Gln	Phe	His	Val	Lys	Ser	Gly	Leu	Gln	Ile	Lys	Lys	Asn	Ala	Ile	
	45					50					55					
atc	gat	gac	tac	aag	gtc	acc	agc	cag	gtc	ctg	ggg	ctg	ggc	atc	aac	603
Ile	Asp	Asp	Tyr	Lys	Val	Thr	Ser	Gln	Val	Leu	Gly	Leu	Gly	Ile	Asn	
60					65					70					75	
ggc	aaa	gtt	ttg	cag	atc	ttc	aac	aag	agg	acc	cag	gag	aaa	ttc	gcc	651
Gly	Lys	Val	Leu	Gln	Ile	Phe	Asn	Lys	Arg	Thr	Gln	Glu	Lys	Phe	Ala	
				80					85					90		
ctc	aaa	atg	ctt	cag	gac	tgc	ccc	aag	gcc	cgc	agg	gag	gtg	gag	ctg	699
Leu	Lys	Met	Leu	Gln	Asp	Cys	Pro	Lys	Ala	Arg	Arg	Glu	Val	Glu	Leu	
			95					100					105			
cac	tgg	cgg	gcc	tcc	cag	tgc	ccg	cac	atc	gta	cgg	atc	gtg	gat	gtg	747
His	Trp	Arg	Ala	Ser	Gln	Cys	Pro	His	Ile	Val	Arg	Ile	Val	Asp	Val	
		110					115					120				
tac	gag	aat	ctg	tac	gca	ggg	agg	aag	tgc	ctg	ctg	att	gtc	atg	gaa	795
Tyr	Glu	Asn	Leu	Tyr	Ala	Gly	Arg	Lys	Cys	Leu	Leu	Ile	Val	Met	Glu	
	125					130					135					
tgt	ttg	gac	ggg	gga	gaa	ctc	ttt	agc	cga	atc	cag	gat	cga	gga	gac	843
Cys	Leu	Asp	Gly	Gly	Glu	Leu	Phe	Ser	Arg	Ile	Gln	Asp	Arg	Gly	Asp	
140					145					150					155	
cag	gca	ttc	aca	gaa	aga	gaa	gca	tcc	gaa	atc	atg	aag	agc	atc	ggg	891
Gln	Ala	Phe	Thr	Glu	Arg	Glu	Ala	Ser	Glu	Ile	Met	Lys	Ser	Ile	Gly	
				160					165					170		
gag	gcc	atc	cag	tat	ctg	cat	tca	atc	aac	att	gcc	cat	cgg	gat	gtc	939
Glu	Ala	Ile	Gln	Tyr	Leu	His	Ser	Ile	Asn	Ile	Ala	His	Arg	Asp	Val	
			175					180					185			
aag	cct	gag	aat	ctc	tta	tac	acc	tcc	aaa	agg	ccc	aac	gcc	atc	ctg	987
Lys	Pro	Glu	Asn	Leu	Leu	Tyr	Thr	Ser	Lys	Arg	Pro	Asn	Ala	Ile	Leu	
		190					195					200				
aaa	ctc	act	gac	ttt	ggc	ttt	gcc	aag	gaa	acc	acc	agc	cac	aac	tct	1035
Lys	Leu	Thr	Asp	Phe	Gly	Phe	Ala	Lys	Glu	Thr	Thr	Ser	His	Asn	Ser	
	205					210					215					
ttg	acc	act	cct	tgt	tat	aca	ccg	tac	tat	gtg	gct	cca	gaa	gtg	ctg	1083
Leu	Thr	Thr	Pro	Cys	Tyr	Thr	Pro	Tyr	Tyr	Val	Ala	Pro	Glu	Val	Leu	
220					225					230					235	
ggg	cca	gag	aag	tat	gac	aag	tcc	tgt	gac	atg	tgg	tcc	ctg	ggg	gtc	1131
Gly	Pro	Glu	Lys	Tyr	Asp	Lys	Ser	Cys	Asp	Met	Trp	Ser	Leu	Gly	Val	
				240					245					250		
atc	atg	tac	atc	ctg	ctg	tgt	ggg	tat	ccc	ccc	ttc	tac	tcc	aac	cac	1179
Ile	Met	Tyr	Ile	Leu	Leu	Cys	Gly	Tyr	Pro	Pro	Phe	Tyr	Ser			

270	275	280	
tat gaa ttt ccc aac cca gaa tgg tca gaa gta tca gag gaa gtg aag			1275
Tyr Glu Phe Pro Asn Pro Glu Trp Ser Glu Val Ser Glu Glu Val Lys			
285	290	295	
atg ctc att cgg aat ctg ctg aaa aca gag ccc acc cag aga atg acc			1323
Met Leu Ile Arg Asn Leu Leu Lys Thr Glu Pro Thr Gln Arg Met Thr			
300	305	310	315
atc acc gag ttt atg aac cac cct tgg atc atg caa tca aca aag gtc			1371
Ile Thr Glu Phe Met Asn His Pro Trp Ile Met Gln Ser Thr Lys Val			
	320	325	330
cct caa acc cca ctg cac acc agc cgg gtc ctg aag gag gac aag gag			1419
Pro Gln Thr Pro Leu His Thr Ser Arg Val Leu Lys Glu Asp Lys Glu			
	335	340	345
cgg tgg gag gat gtc aag ggg tgt ctt cat gac aag aac agc gac cag			1467
Arg Trp Glu Asp Val Lys Gly Cys Leu His Asp Lys Asn Ser Asp Gln			
	350	355	360
gcc act tgg ctg acc agg ttg tga gcagaggatt ctgtgttcct gtccaaactc			1521
Ala Thr Trp Leu Thr Arg Leu *			
	365	370	
agtgtgtgttt cttagaatcc ttttatccccc tgggtctctca atggggacctt aaagaccatc			1581
tggatatcatc ttctcatttt gcagaagaga aactgaggcc cagaggcgga gggcagtctg			1641
ctcaagggtca cgcagctggg gactgggttg ggcagaccgg acccaggttt cctgactcct			1701
ggcccaagtc tcttcctcct atcctgcggg atcactgggg ggctctcagg gaacagcagc			1761
agtgccatag ccaggctctc tgctgccag cgctgggggtg aggctgccgt tgtcagcgtg			1821
gaccactaac cagcccgtct tctctctctg ctcccacccc tgccgcctc accctgccct			1881
tggtgtctct gtctctcacg tctctcttct gctgtctctc ctacctgtct tctggctctc			1941
tctgtaccct tctgggtgct gccgtgcccc caggaggaga tgaccagtgc cttggccaca			2001
atgcgcgttg actacgagca gatcaagata aaaaagattg aagatgcac caaccctctg			2061
ctgctgaaga ggcggaagaa agctcggggc ctggaggctg cggctctggc ccactgagcc			2121
accgcgcct cctgcccacg ggaggacaag caataactct ctacaggaat atatttttta			2181
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 <212> PRT
 <213> Homo sapiens

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 Pro Ala Pro Pro Pro Gln Pro Pro Thr Pro Ala Leu Pro His Pro Pro
 20 25 30
 Ala Gln Pro Pro Pro Pro Pro Gln Gln Phe Pro Gln Phe His Val
 35 40 45
 Lys Ser Gly Leu Gln Ile Lys Lys Asn Ala Ile Ile Asp Asp Tyr Lys
 50 55 60
 Val Thr Ser Gln Val Leu Gly Leu Gly Ile Asn Gly Lys Val Leu Gln
 65 70 75 80
 Ile Phe Asn Lys Arg Thr Gln Glu Lys Phe Ala Leu Lys Met Leu Gln

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      85      90      95
Asp Cys Pro Lys Ala Arg Arg Glu Val Glu Leu His Trp Arg Ala Ser
      100      105      110
Gln Cys Pro His Ile Val Arg Ile Val Asp Val Tyr Glu Asn Leu Tyr
      115      120      125
Ala Gly Arg Lys Cys Leu Leu Ile Val Met Glu Cys Leu Asp Gly Gly
      130      135      140
Glu Leu Phe Ser Arg Ile Gln Asp Arg Gly Asp Gln Ala Phe Thr Glu
145      150      155      160
Arg Glu Ala Ser Glu Ile Met Lys Ser Ile Gly Glu Ala Ile Gln Tyr
      165      170      175
Leu His Ser Ile Asn Ile Ala His Arg Asp Val Lys Pro Glu Asn Leu
      180      185      190
Leu Tyr Thr Ser Lys Arg Pro Asn Ala Ile Leu Lys Leu Thr Asp Phe
      195      200      205
Gly Phe Ala Lys Glu Thr Thr Ser His Asn Ser Leu Thr Thr Pro Cys
      210      215      220
Tyr Thr Pro Tyr Tyr Val Ala Pro Glu Val Leu Gly Pro Glu Lys Tyr
225      230      235      240
Asp Lys Ser Cys Asp Met Trp Ser Leu Gly Val Ile Met Tyr Ile Leu
      245      250      255
Leu Cys Gly Tyr Pro Pro Phe Tyr Ser Asn His Gly Leu Ala Ile Ser
      260      265      270
Pro Gly Met Lys Thr Arg Ile Arg Met Gly Gln Tyr Glu Phe Pro Asn
      275      280      285
Pro Glu Trp Ser Glu Val Ser Glu Glu Val Lys Met Leu Ile Arg Asn
      290      295      300
Leu Leu Lys Thr Glu Pro Thr Gln Arg Met Thr Ile Thr Glu Phe Met
305      310      315      320
Asn His Pro Trp Ile Met Gln Ser Thr Lys Val Pro Gln Thr Pro Leu
      325      330      335
His Thr Ser Arg Val Leu Lys Glu Asp Lys Glu Arg Trp Glu Asp Val
      340      345      350
Lys Gly Cys Leu His Asp Lys Asn Ser Asp Gln Ala Thr Trp Leu Thr
      355      360      365
Arg Leu
      370

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 <212> DNA
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<220>
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 <222> (628)...(831)

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ctgccttggt tctatttttt tatttttttg catcagtatt aatgtttttg catactctcc 180
atctttatcc aaaaatgtaa acttcctttg tcaatctatg gatatgccca tatatgaaag 240
agatgggtgg gtcaaaaagg gatatcaaat gaagtgatag gggtcacaat ggggaaatgg 300
aagtgggtaca taacattgcc aaaataatgt gccactagaa atggtgtaaa ggctgtcttt 360
ttttttaaga aaagttatta ccatgtatgt tgtgaggcag gtttacaaca ctacaagtct 420
tgactaagaa ggaaagagga aaaaagaaaa aacaccaata cccatattta aaaaaaaaaa 480

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aatgatcata gtcttaggag ttcattttaa ccataggaac ttttcactta tctcatgtta 540
 ggtgtaccag tcagtgatta agtagaacta caagttatat aggctgtatt gtttattgct 600
 ggtttatgac cttaataaag tgtaatt atg tat tac cag cag ggt gtt ttt aac 654
 Met Tyr Tyr Gln Gln Gly Val Phe Asn

1 5

tgt gac tat tgt ata aaa aca aat ctt gat atc cag aag cac atg aag 702
 Cys Asp Tyr Cys Ile Lys Thr Asn Leu Asp Ile Gln Lys His Met Lys
 10 15 20 25

ttt gcg act ttc cac cct gcc cat ttt tgt aaa act gca gtc atc ttg 750
 Phe Ala Thr Phe His Pro Ala His Phe Cys Lys Thr Ala Val Ile Leu
 30 35 40

gac ctt tta aac aca aat ttt aaa ctc aac caa gct gtg ata agc gga 798
 Asp Leu Leu Asn Thr Asn Phe Lys Leu Asn Gln Ala Val Ile Ser Gly
 45 50 55

atg gtt act gtt tat act gtg gta tgt ttt tga ttacagcaga taatgctttc 851
 Met Val Thr Val Tyr Thr Val Val Cys Phe *
 60 65

ttttccagtc atctttgaga ataaaggaaa aaaaaaatct tcagatgcaa tggttttgtg 911
 tagcatcttg tctatcatgt tttgtaaatg ctggagaagc gtcgaccaat ttgacttaga 971
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 Lys Leu Asn Gln Ala Val Ile Ser Gly Met Val Thr Val Tyr Thr Val
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 Val Cys Phe
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ctctgcccc cttctatcctt gatacaacag ctgacctcat tteccgatac cttttcccc 300
ccgaaaagta caacatctgg cccgccccag cccgaagaca gcccgctctc cctggacaat 360
cagacgaatt ctcccccccc ccccaaaaaa aaaagccatc cccccgctct gcccgctcgc 420
acattcggcc cccgcgactc ggccagagcg gcgctggcag aggagtgtcc ggcaggaggg 480
ccaacgcccg ctgttcgggt tgcgacacgc agcagggagg tgggcggcag cgtcgccggc 540
ttccagacac ca atg gga atc cca atg ggg aag tgc atg ctg gtg ctt ctc 591
      Met Gly Ile Pro Met Gly Lys Ser Met Leu Val Leu Leu
            1              5              10

acc ttc ttg gcc ttc gcc tcg tgc tgc att gct gct tac cgc ccc agt 639
Thr Phe Leu Ala Phe Ala Ser Cys Cys Ile Ala Ala Tyr Arg Pro Ser
      15              20              25

gag acc ctg tgc ggc ggg gag ctg gtg gac acc ctc cag ttc gtc tgt 687
Glu Thr Leu Cys Gly Gly Glu Leu Val Asp Thr Leu Gln Phe Val Cys
      30              35              40              45

ggg gac cgc ggc ttc tac ttc agc agg ccc gca agc cgt gtg agc cgt 735
Gly Asp Arg Gly Phe Tyr Phe Ser Arg Pro Ala Ser Arg Val Ser Arg
            50              55              60

cgc agc cgt ggc atc gtt gag gag tgc tgt ttc cgc agc tgt gac ctg 783
Arg Ser Arg Gly Ile Val Glu Glu Cys Cys Phe Arg Ser Cys Asp Leu
            65              70              75

gcc ctc ctg gag acg tac tgt gct acc ccc gcc aag tcc gag agg gac 831
Ala Leu Leu Glu Thr Tyr Cys Ala Thr Pro Ala Lys Ser Glu Arg Asp
            80              85              90

gtg tcg acc cct ccg acc gtg ctt ccg gac aac ttc ccc aga tac ccc 879
Val Ser Thr Pro Pro Thr Val Leu Pro Asp Asn Phe Pro Arg Tyr Pro
            95              100              105

gtg ggc aag ttc ttc caa tat gac acc tgg aag cag tcc acc cag cgc 927
Val Gly Lys Phe Phe Gln Tyr Asp Thr Trp Lys Gln Ser Thr Gln Arg
      110              115              120              125

ctg cgc agg ggc ctg cct gcc ctc ctg cgt gcc cgc cgg ggt cac gtg 975
Leu Arg Arg Gly Leu Pro Ala Leu Leu Arg Ala Arg Arg Gly His Val
            130              135              140

ctc gcc aag gag ctc gag gcg ttc agg gag gcc aaa cgt cac cgt ccc 1023
Leu Ala Lys Glu Leu Glu Ala Phe Arg Glu Ala Lys Arg His Arg Pro
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Leu Ile Ala Leu Pro Thr Gln Asp Pro Ala His Gly Gly Ala Pro Pro
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Glu Met Ala Ser Asn Arg Lys *
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 Gly Ile Val Glu Glu Cys Cys Phe Arg Ser Cys Asp Leu Ala Leu Leu
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 Glu Thr Tyr Cys Ala Thr Pro Ala Lys Ser Glu Arg Asp Val Ser Thr
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 Pro Pro Thr Val Leu Pro Asp Asn Phe Pro Arg Tyr Pro Val Gly Lys
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 Phe Phe Gln Tyr Asp Thr Trp Lys Gln Ser Thr Gln Arg Leu Arg Arg
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 Gly Leu Pro Ala Leu Leu Arg Ala Arg Arg Gly His Val Leu Ala Lys
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 Glu Leu Glu Ala Phe Arg Glu Ala Lys Arg His Arg Pro Leu Ile Ala
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 Leu Pro Thr Gln Asp Pro Ala His Gly Gly Ala Pro Pro Glu Met Ala
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 Ser Asn Arg Lys
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